SEQUENCE LISTING

(110) Loughney, Kate

(120) Phosphodiesterase 10

(130) 27866/35308

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(141) 1999-02-23

(150) 60/075,508
(151) 1998-02-23

(160) 36

(170) PatentIn Ver. 2.0

(210) 1
(211) 1548
(212) DNA
(213) Homo sapiens

(220)
(221) CDS
(222) (26)..(1423)

(400) 1

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gccaaggcca tctacctgga catcg atg gac gca ttc aga agc act ccg tac    52
                           Met Asp Ala Phe Arg Ser Thr Pro Tyr
                             1               5

aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta   100
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
 10                  15                  20                  25

atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc   148
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
                 30                  35                  40

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta   196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
             45                  50                  55

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa   244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
         60                  65                  70

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc   292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
     75                  80                  85

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag   340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
 90                  95                 100                 105

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc   388
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
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                                110                 115                 120

tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg     436
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
            125                 130                 135

ctt tcc aag cct aat gag atg ctg agc tgc ctg gag cac atg tac cac     484
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
        140                 145                 150

gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg     532
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg
    155                 160                 165

agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac     580
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His
170                 175                 180                 185

aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc     628
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val
                190                 195                 200

tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc     676
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile
            205                 210                 215

cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac     724
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn
        220                 225                 230

aac aca tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat     772
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn
    235                 240                 245

gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc     820
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile
250                 255                 260                 265

ctc gcc gag cct gag tgc aac atc ttc tct aac atc cca cct gat ggg     868
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly
                270                 275                 280

ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac     916
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp
            285                 290                 295

atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag     964
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu
        300                 305                 310

aat ttt gac tac agc aac gag gag cac atg acc cta ctg aag atg att    1012
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile
    315                 320                 325

ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc    1060
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val
330                 335                 340                 345
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gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc   1108
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
                    350                 355                 360

gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga   1156
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
                365                 370                 375

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc   1204
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
            380                 385                 390

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag   1252
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
        395                 400                 405

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag   1300
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
    410                 415                 420                 425

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac   1348
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
                430                 435                 440

agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat   1396
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
            445                 450                 455

gtg aaa aat agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg         1443
Val Lys Asn Ser Glu Gly Asp Cys Ala
        460                 465

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503

ctgggcacct ggcaccacaa gaccatgttt tctaagaacc atttt                 1548
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<210> 2
<211> 466
<212> PRT
<213> Homo sapiens

<400> 2

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Met Asp Ala Phe Arg Ser Thr Pro Tyr Lys Val Arg Pro Val Ala Ile
  1               5                  10                  15

Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln
             20                  25                  30

Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
         35                  40                  45

Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
     50                  55                  60

Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
 65                  70                  75                  80
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Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
85 90 95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
100 105 110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
115 120 125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
130 135 140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
145 150 155 160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
165 170 175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
180 185 190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
195 200 205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
210 215 220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
225 230 235 240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Gln Asn
245 250 255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
260 265 270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
275 280 285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
290 295 300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
305 310 315 320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
325 330 335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
340 345 350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr

385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
420 425 430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
435 440 445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
450 455 460

Cys Ala
465

<210> 3
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 130, 186, and 205 are either A, T, G, or C.

<400> 3
agcgaccgtg agaagnnaga aggnnttcct gtggaaccgt tcatggaccg agacaaagtg 60

accaaggcca cagcccagat tgggttcatc aagtttgccc tgatcccaat gtttgaaaca 120

gtgaccaagn tcttcnncat ggttgaggag atcatgctgc agccactttg ggaatcccga 180

gatcgntacg aggagctgaa gcggntagat gacgccatga aagag 225

<210> 4
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 12, 36, 61, and 109 are either A, T, G, or C.

<400> 4
gtaccagatc antgcccgca cagagctggc ggtccgntac aatgacatct caccgttgga 60

gnaaccacca ctgcgcngtg gccttccaga tcctcgccga gcctgagtgn aacatcttct 120

ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5
<211> 98
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 14, 23, and 50 are either A, T, C, or G.

<400> 5
gagaacacca ctgngccgtg gnctttcaga tcctcgccga gcctgagtgn aacatctttct 60

tcaacatccc acctgatggg ttcaagcaga tccgacag 98

<210> 6
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 267, 352, 400, and 411 are either A, T, G, or C.

<400> 6
nggttaactg gcgcatcttg tctttctctg agaacagcga tctggttatg gggcatttct 60

gtctctaatg tcactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120

ttcccgtggc ccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180

tttcatcaag tttgrcctga tcccaatgtt tgaaacagtg accaagctch tccccatggg 240

ttgagggaga ttcatgctgg cagccanttt ggggaatccc gaggattcgc tacgagggag 300

cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360

acagttttga agttttgggg gggccaccga ggaagttccn ggaggaggag naggcaga 418

<210> 7
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 82, 92, 130, 347, 390, and 396 are either A, T, G, or C.

<400> 7
nagaaaaaag tgaacaaaat ggttcttaga aaacatggtc ttgtggtgcc aggtgcccag 60

ggagctcttc cctgcacaag gntcccgcgc antcggccag ccgtccaga actgcagcca 120

cgccccccgn tttcctcagg cacagtctcc ttcactgttt ttcacatctc tgcttctctc 180

tctggacttc tcggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240

gggcgtcatc tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300

gcagcatgat cttcctcaac catgggggcg aggagcttgg ggcactngtt ttcaaaaatt 360

gggggatcag gggacaaact ttgattggan cccatnttgg ggcttttggg cctttggggc 420

aatttttg 428

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 63, 93, 107, 188, 203, 206, 238, 252, 297, 370, 389, and 427 are either A, T, G, or C.

<400> 8
ttttttttt ttttttttgt atcagtgaac aaaatggttn ntagaaaaca tggtcttgtg 60

gtnccaggtg cccagggagc tcttccctgc acaaggancn cgcgcantcg gccagcccgt 120

ccagaactgc agccacgccc cccgttttcc tcaggcanag tctccttcac tgtttttcac 180

atctctgntt ctcctctctgg ganttntcgg tgggcccccaq aacgtcaagc tgtcagtntt 240

cttctgtaac tnttttcatgg gcgtcatcta tccgtttcaq cttcctcgta ggcgatnttg 300

gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360

gggtcaattn ttttcaaaac attgggggnt cagggancaa attttgatgg aaacccaatt 420

tggaggntgt gggccttg 438

<210> 9
<211> 262
<212> DNA
<213> Mus musculus

<400> 9
gagaattttg actacagcaa cgaggagcac ctgaccttgt tgaagatgat tctcataaaa 60

tgctgtgata tctccaatga agtccgtccc atggaggtcq cagaatcgtg ggtggactgt 120

ttactggaag aatattttat gcagagtgac cgtgagaaat ccgaagcctt cctgtggccc 180

cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240

tcctgatccc aatgtttgaa ac 262

<210> 10
<211> 250
<212> DNA
<213> Mus musculus

<400> 10
gagaattttg actacagcaa cgaggagcac ctgaccttgt tgaagatgat tctcataaaa 60

tgctgtgata tctccaatga agtccgtccc atggaggtcq cagaatcgtg ggtggactgt 120

ttactaaaag aatattttat gcagagtgac cgtgaggaagt ccgaagcctt ...tgtggccc 180

attcatgaac cgagacaaag tgaccaaagc aacagccaaa ttgggttcat ...aagtttgtc 240

tgtccaatgt 250

<210> 11
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 155, 399, and 443 are either A, T, G, or C.

<400> 11
attaatcttg gccactgaca tggcaagaca tgcaggaatt atggattctt tcaaagagaa 60

aatggaggaat tttgactaca gcaacgagga gcacatgacc ctggtgagtg gcttattctg 120

cctgggtagg cagccaggcg gttgggctgg cgaaaaggtt catccatcca gctcacactg 180

gaagccaaga agctgaaatt attagtcttc ttggaacaag gtgttataa atctggtttt 240

caaggttatg attcttacta ggaaagtccg ggcagtgcct cctcctgat gggtcctcct 300

tcatggtcag aggcagcatt ctcccattcc tccatctctt ttgggatttt gaaggagata 360

aagtgggtg aaggccgtgc attctgctc tgntttcca gagaattaaa accagttttc 420

cattgaaggc acagccccag cntggcattt tgaaagttg 459

<210> 12
<211> 499
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (49)..(443)

<400> 12
tggcctcga ggccaagaat tcggcacgag tggtaactg gcgcatcttg tctttctctg 60

agaacaacga ttggttatg gggcatttct gtct aa tgt cac tgt ctg ctg cat 116
Cys His Cys Leu Leu His
1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
10 15 20

ttc atg gac cga gac aaa gtg acc aag gct aca gcc cag att ggg ttc 212
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
25 30 35

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atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc   160
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
     40                  45                  50

ccc atg gtt gaa gag atc atg ctg cag cca ctt tgg gaa tcc cga gat   208
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
 55                  60                  65                  70

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag   256
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
                 75                  80                  85

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tct aga gag   304
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
             90                  95                 100

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc   353
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
         105                 110                 115

ggggggcgtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 513

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca 573

ctgatacaaa aaaaaaaaaa aaaaaa                                     599
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<210> 13
<211> 115
<212> PRT
<213> Homo sapiens

<400> 13

```
Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu
  1               5                  10                  15

Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala
             20                  25                  30

Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu
         35                  40                  45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
     50                  55                  60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
 65                  70                  75                  80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala
                 85                  90                  95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
            100                 105                 110

Asp Cys Ala
        115
```

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
agtcgaattc acgtgagaa gtcagaag 28

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gtcaaagctt acatggtctt gtggtgcc 28

<210> 16
<211> 1303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (107)..(1066)

<400> 16
agtgactcta ctttgtgaaa atgtgaaact tcgtgtaggt actcagtaaa tcagtaaatt 60

cttactaaag ttagccccca gcctagctat ggagggtgca tgctga gcc ctg gag 115
Ala Leu Glu
1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
40 45 50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
55 60 65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His

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                70                  75                  80

ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg   403
Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala
     85                  90                  95

gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg   451
Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val
100                 105                 110                 115

gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc   499
Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile
                    120                 125                 130

cca ccc gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc   547
Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile
                135                 140                 145

ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa   595
Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys
            150                 155                 160

gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg   643
Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu
        165                 170                 175

ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt   691
Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg
180                 185                 190                 195

cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat   739
Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr
                    200                 205                 210

ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg   787
Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
                215                 220                 225

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc   835
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
            230                 235                 240

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttt   883
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
        245                 250                 255

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat   931
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
260                 265                 270                 275

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag   979
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
                    280                 285                 290

aag aag act gac agc ttg acc tct ggg gcc acc gag aag tcc aaa gag   1027
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Lys Glu
                295                 300                 305
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aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc     1076
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
        310                 315                 320

gggggggcgtg gctgcagttc tggacgggct ggctgagctg cgcgggatcc ttgtgcaggg 1136

aagagctgcc ctgggcacct ggcacacaca gaccatgttt tctaagaacc attttgttca 1196

ctgatacaaa aaaaaaaaag gaattcatga tgctgtacag aatttttattt ttaaactgtc 1256

ttttaaataa tatattctta tacggaaaaa aaaaaaaaaa aaaaaaa                1303
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<210> 17
<211> 320
<212> PRT
<213> Homo sapiens

<400> 17

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Ala Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser
  1               5                  10                  15

Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn
             20                  25                  30

Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala
         35                  40                  45

Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
     50                  55                  60

Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
 65                  70                  75                  80

Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
                 85                  90                  95

Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
            100                 105                 110

Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
        115                 120                 125

Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
    130                 135                 140

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
145                 150                 155                 160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
                165                 170                 175

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
            180                 185                 190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
        195                 200                 205
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Glu Gln Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
    210                 215                 220

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
225                 230                 235                 240

Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
                245                 250                 255

Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
            260                 265                 270

Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
        275                 280                 285

Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys
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Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
305                 310                 315                 320
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cgccgggcgc agg atg gga tcc ggc tcc tcc agc tac cgg ccc aag gcc    109
               Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala
                 1               5                  10

atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag   157
Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
         15                  20                  25

tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc   205
Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
     30                  35                  40

ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg   253
Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met
 45                  50                  55                  60

gtc tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac   301
Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr
                 65                  70                  75

aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta   349
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
             80                  85                  90
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atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc   397
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
         95                  100                 105

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta   445
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
     110                 115                 120

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa   493
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
 125                 130                 135                 140

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc   541
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
                 145                 150                 155

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag   589
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asn Asn His Lys
             160                 165                 170

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc   637
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
         175                 180                 185

tct cca gag act atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg   685
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
     190                 195                 200

ttt tgg gag ccc aat gag atg ctg agc tgc ctg gag cat atg tac cac   733
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
 205                 210                 215                 220

gac ctc ggg ctg gtc agg gac ttc agc atc aac ccc gtg acc ctc agg   781
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg
                 225                 230                 235

agg tgg ctg ttc tgc gtc cac gac aac tac agg aac aac ccg ttc cac   829
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His
             240                 245                 250

aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc   877
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val
         255                 260                 265

tgg ctc tgc agt ctc cag gag aag ttc tca caa atg gat atc ctg atc   925
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Met Asp Ile Leu Ile
     270                 275                 280

cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac   973
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn
 285                 290                 295                 300

aac acg tac cag atc aat gcc cgc aca gag ctg gcc gtc cgc tac aat   1021
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn
                 305                 310                 315

gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc   1069
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile
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                320                 325                 330

ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg  1117
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly
        335                 340                 345

ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac  1165
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp
    350                 355                 360

atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag  1213
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu
365                 370                 375                 380

aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att  1261
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile
                385                 390                 395

ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc  1309
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val
            400                 405                 410

gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc  1357
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
        415                 420                 425

gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga  1405
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
    430                 435                 440

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc  1453
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
445                 450                 455                 460

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag  1501
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
                465                 470                 475

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag  1549
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
            480                 485                 490

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac  1597
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
        495                 500                 505

agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat  1645
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp
    510                 515                 520

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg        1692
Val Lys Asn Ser Glu Gly Asp Cys Ala
525                 530

gctgcagttc tgaacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1752

ctgggcacct aaaaccacaa gaccatgttt tctaagaacc attttgttca ctgataaaaa 1812
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Ile	Asp	Gly	Arg	Ile	Gln	Lys	Val	Ile	Phe	Ser	Lys	Tyr	Cys	Asn	Ser
			20					25					30		
Ser	Asp	Ile	Met	Asp	Leu	Phe	Cys	Ile	Ala	Thr	Gly	Leu	Pro	Arg	Asn
		35					40					45			
Thr	Thr	Ile	Ser	Leu	Leu	Thr	Thr	Asp	Asp	Ala	Met	Val	Ser	Ile	Asp
	50					55					60				
Pro	Thr	Met	Pro	Ala	Asn	Ser	Glu	Arg	Thr	Pro	Tyr	Lys	Val	Arg	Pro
65					70					75					80
Val	Ala	Ile	Lys	Gln	Leu	Ser	Glu	Arg	Glu	Glu	Leu	Ile	Gln	Ser	Val
				85					90					95	
Leu	Ala	Gln	Val	Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	Lys	Ile	Asn	Glu
			100					105					110		
Leu	Lys	Ala	Glu	Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val
		115					120					125			
Glu	Leu	Glu	Gly	Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp
	130					135					140				
Ile	Lys	Lys	Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn
145					150					155					160
Cys	Pro	Cys	Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro
				165					170					175	
Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr
			180					185					190		
Ile	Gln	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro
		195					200					205			
Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu
	210					215					220				
Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe
225					230					235					240
Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His
				245					250					255	

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
420 425 430

Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
435 440 445

Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
450 455 460

Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
485 490 495

Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser
500 505 510

Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser
515 520 525

Glu Gly Asp Cys Ala
530

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<213> Homo sapiens

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<222> (2)..(1741)

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  Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
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tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg 97
Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
            20   25   30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
        35   40   45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
    50   55   60

gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65   70   75   80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
                85   90   95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
            100   105   110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
        115   120   125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
    130   135   140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg 481
Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145   150   155   160

aaa gct gaa gtt gca aat cac tta gct gtc cta gag aaa cgc gtg gaa 529
Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
                165   170   175

ttg gaa gga cta aaa gtg gtg gaa att gag aaa tgc aag agt gac att 577
Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
            180   185   190

aag aag atg agg gag gag ctg gca gcc aga agc agc agg acc aac tgt 625
Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
        195   200   205

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ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga   673
Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
    210                 215                 220

cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag aac atc   721
Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Asn Ile
225                 230                 235                 240

gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat   769
Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
                245                 250                 255

gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc   817
Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
            260                 265                 270

agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc   865
Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
        275                 280                 285

gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc   913
Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
    290                 295                 300

ttc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc   961
Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305                 310                 315                 320

cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca ggg gcc  1009
Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
                325                 330                 335

atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc  1057
Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
            340                 345                 350

aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg  1105
Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
        355                 360                 365

gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag  1153
Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
    370                 375                 380

tgc aac atc ttc tcc aac atc tcg cct gat ggg ttc aag cag atc cga  1201
Cys Asn Ile Phe Ser Asn Ile Ser Pro Asp Gly Phe Lys Gln Ile Arg
385                 390                 395                 400

cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca  1249
Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
                405                 410                 415

gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc  1297
Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
            420                 425                 430

aac gag gag cac atg acc ctt ctg aag atg att ttg ata aaa tgc tgt  1345
Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
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        435                 440                 445

gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg   1393
Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
    450                 455                 460

gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca   1441
Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465                 470                 475                 480

gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag   1489
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
                485                 490                 495

gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt   1537
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
            500                 505                 510

gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag   1585
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
        515                 520                 525

cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cag ata gat   1633
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
    530                 535                 540

gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg   1681
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
545                 550                 555                 560

gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa   1729
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
                565                 570                 575

gga gac tgt gcc tgaggaaagc gggggggcgtg gctgcagttc tggacgggct      1781
Gly Asp Cys Ala
            580

ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa 1841

gaccatgttt tctaagaacc attttgttca ctgatacaaa aaaaaaaaaa ggaattcatg 1901

atgctgtaca gaattttatt tttaaactgt cttttaaata atatattctt atacggaaaa 1961

aaaaaa                                                            1967
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<210> 21
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<400> 21

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Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
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Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
             20                  25                  30
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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
180 185 190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
195 200 205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
210 215 220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
225 230 235 240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
245 250 255

Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
260 265 270

Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
275 280 285

Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
290 295 300

Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305 310 315 320

Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
325 330 335

Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile

340 345 350

Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
355 360 365

Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
370 375 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
385 390 395 400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
405 410 415

Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
420 425 430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
435 440 445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
450 455 460

Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465 470 475 480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
485 490 495

Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
500 505 510

Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
515 520 525

Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
530 535 540

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Gly Asp Cys Ala
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cgccccccgc ccgccccctc ccctgctccc rtccccccgcc tcccgcggcg gctggcgtcg 120

ggaaagtaca gtaaaaagtc cgagtgcagc cgccgggcgc agg atg gga tcc ggc   175
                                                Met Gly Ser Gly
                                                  1

tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc   223
Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
  5                  10                  15                  20

att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg   271
Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met
                 25                  30                  35

gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc   319
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser
             40                  45                  50

ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc   367
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro
         55                  60                  65

gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag   415
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys
     70                  75                  80

caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt   463
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
 85                  90                  95                 100

gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa   511
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
                105                 110                 115

gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga   559
Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly
            120                 125                 130

cta aaa gtg gtg gag att gag aaa tgc aag agt gac att aag aag atg   607
Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met
        135                 140                 145

agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc ccc tgt aag   655
Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys
    150                 155                 160

tac agt ttt ttg gat aac cac aag aag ttg act cct cga cgc gat gtt   703
Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val
165                 170                 175                 180

ccc act tac ccc aag tac ctg ctc tct cca gag acc atc gag gcc ctg   751
Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu
                185                 190                 195

cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat gag atg ctg   799
Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu
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                200                 205                 210

agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc agg gac ttc   847
Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe
        215                 220                 225

agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac   895
Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp
    230                 235                 240

aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg   943
Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val
245                 250                 255                 260

gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc cag gag aag   991
Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys
                265                 270                 275

ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc atc tgc cac  1039
Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His
            280                 285                 290

gat ctg gac cat ccc ggc tac aac aac acg tac cag atc aat gcc cgc  1087
Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg
        295                 300                 305

aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg gag aac cac  1135
Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His
    310                 315                 320

cac tgc gcc gtg gcc ttc cag atc ctc cag gag ccc gag tgc aac atc  1183
His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
325                 330                 335                 340

ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga cag gga atg  1231
Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
                345                 350                 355

atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg  1279
Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
            360                 365                 370

gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag  1327
Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
        375                 380                 385

cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct  1375
His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
    390                 395                 400

aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta  1423
Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
405                 410                 415                 420

tta gag gaa tat ttt atg cag agc gac cgt gaga                     1457
Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
                425                 430
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<213> Homo sapiens

<400> 23

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Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
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Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
            20                  25                  30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
        35                  40                  45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
    50                  55                  60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
65                  70                  75                  80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
                85                  90                  95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
            100                 105                 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
        115                 120                 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
    130                 135                 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
145                 150                 155                 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
                165                 170                 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
            180                 185                 190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
        195                 200                 205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
    210                 215                 220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
225                 230                 235                 240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
                245                 250                 255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
            260                 265                 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
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275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
340 345 350

Arg Glu Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
355 360 365

Ala Gln Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
420 425 430

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Asp Thr Lys Asp Asp Asp Asp Lys
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tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact 54

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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cgaggagtca acttctg 17